



SEQUENCE LISTING

<110> Kindsvogel, Wayne R.
Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827

<151> 2000-08-08

<150> US 60/250,876

<151> 2000-12-01

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<170> FastSEQ for Windows Version 3.0

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<211> 2831

<212> DNA

<213> Homo sapien

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<221> CDS

<222> (34)...(1755)

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Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp	
10 15 20	
ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg	150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu	
25 30 35	
acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc	198

Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile	
40 45 50 55	
gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt	246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys	
60 65 70	
cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac	294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn	
75 80 85	
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc	342
Ileu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly	
90 95 100	
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act	390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr	
105 110 115	
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att	438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile	
120 125 130 135	
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc	486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly	
140 145 150	
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta	534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu	
155 160 165	
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag	582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln	
170 175 180	
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc	630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly	
185 190 195	
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac	678
Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr	
200 205 210 215	

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Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe	
220 225 230	
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Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	
235 240 245	
tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc	822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	
250 255 260	
ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag	870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	
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gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg	918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	
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gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag	966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	
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ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta	1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	
315 320 325	
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Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
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Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
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Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
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Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
380 385 390	

cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met 395 400 405	1254
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gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys 460 465 470	1446
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gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc	1734

Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
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<213> Homo sapien

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 20 25 30
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 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val

				85					90					95	
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg
			100					105						110	
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys
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Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr
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Pro	Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe
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His	Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln
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Met	His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr
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Pro	Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp
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Ala	Lys	Glu	Ser	Ala	Pro	Tyr	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp
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Phe	Leu	Val	Ala	Val	Leu	Cys	Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys
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Pro	Pro	Ala	Pro	Pro	Asn	Ser	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe
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Gln	Pro	Leu	Arg	Phe	Ile	Gln	Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp
	275						280					285			
Leu	Ser	Gly	Pro	Ser	Ser	Leu	Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile
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Arg	Val	Ser	Gly	Pro	Arg	Glu	Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser
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Leu	Ser	Glu	Ile	Thr	Tyr	Leu	Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln
			325					330					335		
Pro	Ser	Asn	Val	Pro	Pro	Pro	Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala
			340					345					350		
Pro	Asn	Ala	Ala	Pro	Glu	Val	Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val
	355						360					365			
Thr	Pro	Glu	Ala	Gln	Phe	Pro	Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys
	370					375					380				
Val	Gln	Pro	Ser	Ser	Tyr	Ala	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro
385					390					395					400
Pro	Ser	Tyr	Gly	Val	Cys	Met	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr
			405					410						415	
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Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
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<212> PRT

<213> Homo sapiens

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 20 25 30
 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
 35 40 45
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
 50 55 60
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
 65 70 75 80
 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
 85 90 95
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
 100 105 110
 Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
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 130 135 140

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<220>
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<212> PRT
<213> Artificial Sequence

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<223> Flag-tag peptide
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<?12> DNA
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aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc ctcctccat cgagaaaacc 360
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gatgagctga ccaagaacca ggtcagcctg acctgcttg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
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<213> homo sapiens

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ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg 101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
          15             20             25

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gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac 149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
          30             35             40

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aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg 197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
          45             50             55

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gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att 245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
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atg	aag	cag	gtg	ctg	aac	ttc	acc	ctt	gaa	gaa	gtg	ctg	ttc	cct	caa	341
Met	Lys	Gln	Val	Leu	Asn	Phe	Thr	Leu	Glu	Glu	Val	Leu	Phe	Pro	Gln	
		95						100					105			
tct	gat	agg	ttc	cag	cct	tat	atg	cag	gag	gtg	gtg	ccc	ttc	ctg	gcc	389
Ser	Asp	Arg	Phe	Gln	Pro	Tyr	Met	Gln	Glu	Val	Val	Pro	Phe	Leu	Ala	
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agg	ctc	agc	aac	agg	cta	agc	aca	tgt	cat	att	gaa	ggt	gat	gac	ctg	437
Arg	Leu	Ser	Asn	Arg	Leu	Ser	Thr	Cys	His	Ile	Glu	Gly	Asp	Asp	Leu	
	125					130					135					
cat	atc	cag	agg	aat	gtg	caa	aag	ctg	aag	gac	aca	gtg	aaa	aag	ctt	485
His	Ile	Gln	Arg	Asn	Val	Gln	Lys	Leu	Lys	Asp	Thr	Val	Lys	Lys	Leu	
140				145					150					155		
gga	gag	agt	gga	gag	atc	aaa	gca	att	gga	gaa	ctg	gat	ttg	ctg	ttt	533
Gly	Glu	Ser	Gly	Glu	Ile	Lys	Ala	Ile	Gly	Glu	Leu	Asp	Leu	Leu	Phe	
			160					165					170			
atg	tct	ctg	aga	aat	gcc	tgc	att	tgaccagagc	aaagctgaaa	aatgaataac						587
Met	Ser	Leu	Arg	Asn	Ala	Cys	Ile									
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aaacccctaa	atagcttcat	gtttccataa	tcagtacttt	atatttataa	atgtatttat											947
tattattata	agactgcatt	ttatttatat	cattttatta	atatggattt	atttatagaa											1007
acatcattcg	atattgttac	ttgagtgtaa	ggctaataat	gatatttatg	acaataatta											1067
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<210> 8

<211> 179

<212> PRT

<213> homo sapiens

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 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide prime ZC28590

<400> 9

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36

<210> 10

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<223> Oligonucleotide prime ZC28580

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 <223> Oligonucleotide prime ZC14666

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 agccaccaag atgactga 18

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 <223> Oligonucleotide prime ZC14742

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<210> 13
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 <212> PRT
 <213> Artificial Sequence

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 <223> His tag

<400> 13
 His His His His His His
 1 5

<210> 14
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 <212> DNA
 <213> Artificial Sequence

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<223> Oligonucleotide primer ZC29239

<400> 14

gaggccgcat cgggttcggg ttcgggttcg gagccagat catcagacaa aactcacaca	60
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<211> 65

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC29232

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cgactgactc gactcagtga tggatgatgg gatggccacc tgatccttta cccggagaca	60
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<223> Oligonucleotide primer ZC39319

<400> 16

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<210> 17

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<212> DNA

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<223> Oligonucleotide primer ZC39325

<400> 17

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<210> 18

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(660)

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1 5 10 15	
gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt	96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val	
20 25 30	
aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg	144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly	
35 40 45	
aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat	192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp	
50 55 60	
aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc	240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser	
65 70 75 80	
aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag	288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu	
85 90 95	
cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att	336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile	
100 105 110	
att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat	384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His	
115 120 125	
atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act	432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr	
130 135 140	

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc 624
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc 660
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 19

<211> 220

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38931

<400> 20

acaaagccgc gggaggag

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<210> 21

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39042

<400> 21

ctgactcag tcagtgatgg tgatggtgat ggccacctga tccggaacca cgcggaacca
 gttaccctgg agacagggag ag

60

82

<210> 22

<211> 1428

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused
to IgG1 with a 6-HIS tag

<400> 22

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Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser	
1				5				10				15				

gca	ttg	gga	atg	gta	cca	cct	ccc	gaa	aat	gtc	aga	atg	aat	tct	gtt	96
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	
			20					25				30				

aat	ttc	aag	aac	att	cta	cag	tgg	gag	tca	cct	gct	ttt	gcc	aaa	ggg	144
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	
		35					40					45				

aac	ctg	act	ttc	aca	gct	cag	tac	cta	agt	tat	agg	ata	ttc	caa	gat	192
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	
	50					55					60					

aaa	tgc	atg	aat	act	acc	ttg	acg	gaa	tgt	gat	ttc	tca	agt	ctt	tcc	240
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	
65					70					75				80		

aag	tat	ggt	gac	cac	acc	ttg	aga	gtc	agg	gct	gaa	ttt	gca	gat	gag	288
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	
			85					90					95			

cat	tca	gac	tgg	gta	aac	atc	acc	ttc	tgt	cct	gtg	gat	gac	acc	att	336
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
		100					105					110				

att	gga	ccc	cct	gga	atg	caa	gta	gaa	gta	ctt	gat	gat	tct	tta	cat	384
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
	115					120					125					

atg	cgt	ttc	tta	gcc	cct	aaa	att	gag	aat	gaa	tac	gaa	act	tgg	act	432
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	
130						135					140					

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa	480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys	
145 150 155 160	
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag	528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu	
165 170 175	
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga	576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg	
180 185 190	
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc	624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val	
195 200 205	
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg	672
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser	
210 215 220	
ggt tcg ggt tcg gag ccc aga tca tca gac aaa act cac aca tgc cca	720
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro	
225 230 235 240	
ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc	768
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe	
245 250 255	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	816
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
260 265 270	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	864
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
275 280 285	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	912
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
290 295 300	
ccg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	960

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
305 310 315 320	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1008
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
325 330 335	
tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc	1056
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala	
340 345 350	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	1104
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
355 360 365	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1152
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
370 375 380	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1200
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
385 390 395 400	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc	1248
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
405 410 415	
ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag	1296
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
420 425 430	
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac	1344
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	
435 440 445	
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt	1392
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg	
450 455 460	
ggt tcc gga tca ggt ggc cat cac cat cac cat cac	1428
Gly Ser Gly Ser Gly Gly His His His His His His	
465 470 475	

<210> 23
 <211> 476
 <212> PRT
 <213> Homo sapiens

<400> 23

Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser
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Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val
			20					25					30		
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly
		35					40					45			
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Ile	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp
		50				55					60				
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser
65					70					75					80
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu
			85					90						95	
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile
			100					105					110		
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His
		115				120						125			
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr
		130				135						140			
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys
145					150					155					160
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu
			165					170						175	
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Tyr	Cys	Val	Gln	Val	Arg	
		180						185				190			
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val
		195					200					205			
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser	Gly	Ser	Gly	Ser
		210				215						220			
Gly	Ser	Gly	Ser	Glu	Pro	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro
225					230					235					240
Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe
			245					250					255		
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
		260						265					270		
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
		275					280					285			

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 290 295 300
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 305 310 315 320
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 325 330 335
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 340 345 350
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 355 360 365
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 370 375 380
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 385 390 395 400
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 405 410 415
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 420 425 430
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 435 440 445
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
 450 455 460
 Gly Ser Gly Ser Gly Gly His His His His His His
 465 470 475

<210> 24

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29328

<400> 24

tcagagggat cgggttcggg ttccgggttcg gagcccagat catcagacaa aactcacaca
 tgc

60

63

<210> 25

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29231

<400> 25

cgactgactc gagctactcc ataggcatat actgccacc tgatccttta cccggagaca 60
gggag 65

<210> 26

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39335

<400> 26

atcggaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60
tgctcacgcc 70

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28981

<400> 27

tttgggctcc ctgagctctg gtggaa 26

<210> 28

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39043

<400> 28

ctgactcgag ctactccata ggcataact cgccacctga tccggaacca cgcggaacca 60
gtttaccagg agacagggag 80

<210> 29

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<223> hzcytor11 extracellular cytokine binding domain
fused to IgG1 with a Glu-Glu tag

<221> CDS

<222> (1)...(1452)

<400> 29

atg	agg	acg	ctg	ctg	acc	atc	ttg	act	gtg	gga	tcc	ctg	gct	gct	cac	48
Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His	
1			5						10					15		

gcc	cct	gag	gac	ccc	tcg	gat	ctg	ctc	cag	cac	gtg	aaa	ttc	cag	tcc	96
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	
			20					25					30			

agc	aac	ttt	gaa	aac	atc	ctg	acg	tgg	gac	agc	ggg	cca	gag	ggc	acc	144
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	
	35					40					45					

cca	gac	acg	gtc	tac	agc	atc	gag	tat	aag	acg	tac	gga	gag	agg	gac	192
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	
	50					55					60					

tgg	gtg	gca	aag	aag	ggc	tgt	cag	cgg	atc	acc	cgg	aag	tcc	tgc	aac	240
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	
65					70				75					80		

ctg	acg	gtg	gag	acg	ggc	aac	ctc	acg	gag	ctc	tac	tat	gcc	agg	gtc	288
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	
			85					90					95			

acc	gct	gtc	agt	gcg	gga	ggc	cgg	tca	gcc	acc	aag	atg	act	gac	agg	336
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	
			100				105					110				

ttc	agc	tct	ctg	cag	cac	act	acc	ctc	aag	cca	cct	gat	gtg	acc	tgt	384
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	
	115					120						125				

atc tcc aaa gtg aga tgg att cag atg att gtt cat cct acc ccc acg Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr 130 135 140	432
cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe 145 150 155 160	480
cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln 165 170 175	528
atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr 180 185 190	576
cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp 195 200 205	624
gcc aag gag agt gcc ccc tac atg tgc cga gtg aag aca ctg cca gac Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp 210 215 220	672
cgg aca tgg acc gga tcc ggt tgg ggt tgg ggt tgg gag ccc aga tca Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser 225 230 235 240	720
tca gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu 245 250 255	768
ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 260 265 270	816
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 275 280 285	864
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac gcc gtg gag His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 290 295 300	912

gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg	960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
305 310 315 320	
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
325 330 335	
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc	1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser	
340 345 350	
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag	1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	
355 360 365	
gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc	1152
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val	
370 375 380	
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg	1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val	
385 390 395 400	
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct	1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro	
405 410 415	
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc	1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr	
420 425 430	
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg	1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val	
435 440 445	
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg	1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu	
450 455 460	
tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat	1440

Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480

atg cct atg gag
 Met Pro Met Glu

1452

<210> 30
 <211> 484
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hzcytor11 extracellular cytokine binding domain
 fused to IgG1 with a Glu-Glu tag

<400> 30
 Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
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 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
 85 90 95
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
 100 105 110
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190

Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
 225 230 235 240
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
 245 250 255
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480
 Met Pro Met Glu

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22

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23

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<211> 199

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<213> Homo sapiens

<400> 33

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Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr
		20						25					30		
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met
		35					40					45			
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly
		50				55					60				
Asp	His	Thr	Ile	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp
65				70				75					80		
Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro
			85					90					95		
Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe
		100					105					110			
Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn
		115				120					125				
Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr
		130				135					140				

Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
 180 185 190
 Thr Thr His Asp Glu Thr Val
 195

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<400> 34
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 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
 85 90 95
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
 100 105 110
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
 130 135 140
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
 145 150 155 160
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
 165 170 175
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
 180 185 190
 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
 195 200 205
 Thr Arg Gln
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 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
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 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
 35 40 45
 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
 50 55 60
 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
 65 70 75 80
 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
 85 90 95
 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
 100 105 110
 Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
 115 120 125
 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
 130 135 140
 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
 145 150 155 160
 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
 165 170 175
 Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
 180 185 190
 Glu Cys Val Glu Val Gln Gly Glu Ala
 195 200